The genome of the rubber tree (*Hevea brasiliensis*)

Marc Seguin

UMR DAP, CIRAD, France

ABSTRACT

Rubber tree (*Hevea brasiliensis*) is a member of the family Euphorbiaceae, sub-family articulated crotonoids. The 10 species of the genus *Hevea* have 2n = 36 chromosomes and there has been a suggestion of allotetraploidy with x = 9, but genome mapping of hundreds of genetic markers revealed only disomic segregations in *H. brasiliensis*. Restriction fragment length polymorphism (RFLP) mapping allowed revealing 10 duplicated chromosome segments, but there is no clear evidence of multivalent pairings during meiosis. Consequently, *Hevea* species have to be considered as diploids with 2n = 2x = 36. Status of the genome of *Manihot*, a genus phylogenetically close to *Hevea* and belonging to the same botanical sub-family, is very similar with 2n = 36 chromosomes for all *Manihot* species, including cassava (*Manihot esculenta*). In contrast, despite these similarities, the nuclear genomes of rubber tree and cassava differ greatly in size, with a haploid genome (1 C) of 2,100 mega bases (Mb) in *H. brasiliensis* and of 800 Mb in *M. esculenta*. It can be postulated that this genome size difference is mainly attributable to the amount of repetitive DNA which constitutes probably more than 64 % of the *Hevea* nuclear genome, and that conversely the single/low copy fraction, encompassing the transcribed regions, probably represents less than 750 Mb in this species. Therefore, whole genome sequencing of rubber tree will be a tremendous task. New DNA sequencing technologies theoretically open to the possibility obtaining a draft sequence of the whole genome even for large genome species. Obviously, it would be useful to concentrate DNA sequencing effort on the low single/copy fraction in order to avoid wasting time and money in repetitive DNA sequencing. But, even in this case, a whole genome sequencing work would first produce a huge number of unarranged small contigs, and after this first step, a great amount of work in physical mapping will be necessary. Moreover, sequence contig assembly is complicated in case of heterozygous species, and all *Hevea* accessions are highly heterozygous genotypes. Nevertheless, whole genome sequencing of cassava is currently in progress, and because a strong synteny between rubber tree and cassava genomes is expected, the sequence alignment between the 2 species will be of great benefit for a genome sequencing project in rubber tree.